

SEQUENCE LISTING

<110> UAB Research Foundation

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<120> METHODS AND COMPOSITIONS FOR IDENTIFYING
COMPOUNDS THAT INHIBIT HIV-1 SUBUNIT-SPECIFIC REVERSE
TRANSCRIPTASE

<130> 21085.0123P1

<140> Unassigned
<141> 2005-05-24

<150> 60/573,918
<151> 2004-05-24

<150> 60/668,858
<151> 2005-04-06

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 858
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 1
gtttaaacgc caccatggag caggcccccg aggaccaggg cccccagagg gagccccaca 60
acgagtggac cctggagctg ctggaggagc tgaagaggga ggccgtgagg cacttccccca 120
ggccctggct gcacggcctg ggccagcaca tctacgagac ctacggcgac acctggcccg 180
gcgtggagc catcatcagg atcctgcagc agctgctgtt catccacttc aggatcggtct 240
gccagcacag caggatcgcc atcatccagc agaggaggc caggaggaac ggcgccagca 300
ggagctagtt taaacactgc acagagagac aggttaattt tttagggaaa atttggcctt 360
ccaacaaaagg gaggccaggg aattttctcc agaacaggcc agagccaaca gccccaccccg 420
cagagacgtt cgggttcgga gaggagatag cccctcccc gaaacaagag ccgaaggaaa 480
aggagttata ccccttaacc tccctcaaat cactcttgg cagcgacccc tagtcacagt 540
agaataggg ggcacagctaa tagaaggcct gtttagacaca ggagcagatg atacagtgtt 600
agaagatata aatttaccag gaaaatggaa accaaaaatg atagggggaa ttggtggtct 660
tatcaaagta agacagtatg atcaaatact tatagaaatt tgtggaaaaa aggctatagg 720
gacagtatata gtaggaccta cacctatcaa cataattggg agaaatatgt tgactcagat 780
tggttgtact ttaaatttc caattagtcc tattgaaact gtaccagtaa aattaaagcc 840
aggaatggat ggtccaaa 858

<210> 2
<211> 96
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 2

Met Glu Gln Ala Pro Glu Asp Gln Gly Pro Pro Arg Glu Pro Tyr Asn
1 5 10 15
Ala Trp Thr Leu Glu Leu Leu Glu Glu Leu Lys Ser Glu Ala Val Arg
20 25 30
His Phe Pro Arg Val Trp Leu His Gly Leu Gly Gln His Ile Tyr Glu
35 40 45
Thr Tyr Gly Asp Thr Trp Ala Gly Val Glu Ala Ile Ile Arg Ile Leu
50 55 60
Gln Gln Leu Leu Phe Ile His Phe Arg Ile Gly Cys Gln His Ser Arg
65 70 75 80
Ile Gly Ile Thr Arg Gln Arg Arg Ala Arg Asn Gly Ala Ser Arg Ser
85 90 95

<210> 3

<211> 315
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 3

gtttaaacgc	caccatggag	caggcccccg	aggaccaggg	cccccagagg	gagccccaca	60
acgagtgac	cctggagctg	ctggaggagc	tgaagaggga	ggccgtgagg	cacttcccca	120
ggccctggct	gcacggcctg	ggccagcaca	tctacgagac	ctacggcgac	acctggcccg	180
gcgtggaggc	catcatcagg	atcctgcagc	agctgctgtt	catccacttc	agatcggct	240
gccagcacag	caggatcgcc	atcatccagc	agaggagggc	caggaggaac	ggcgccagca	300
ggagctagtt	taaac					315

<210> 4

<211> 440
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 4

Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
1 5 10 15
Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys
20 25 30
Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
35 40 45
Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys
50 55 60
Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
65 70 75 80
Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
85 90 95
Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
100 105 110
Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr
115 120 125

Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160
 Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
 165 170 175
 Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
 180 185 190
 Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His
 195 200 205
 Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu
 210 215 220
 Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
 225 230 235 240
 Val Gln Pro Ile Val Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
 245 250 255
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro
 260 265 270
 Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
 275 280 285
 Leu Thr Glu Val Ile Pro Leu Thr Glu Ala Glu Leu Glu Leu Ala
 290 295 300
 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
 305 310 315 320
 Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln
 325 330 335
 Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
 340 345 350
 Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu
 355 360 365
 Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
 370 375 380
 Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr
 385 390 395 400
 Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe
 405 410 415
 Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu
 420 425 430
 Pro Ile Val Gly Ala Glu Thr Phe
 435 440

<210> 5

<211> 440

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 5

Pro Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met
 1 5 10 15
 Asp Gly Pro Lys Val Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys
 20 25 30
 Ala Leu Val Glu Ile Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser
 35 40 45
 Lys Ile Gly Pro Glu Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys
 50 55 60
 Lys Lys Asp Ser Thr Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu
 65 70 75 80

Asn Lys Arg Thr Gln Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His
 85 90 95
 Pro Ala Gly Leu Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly
 100 105 110
 Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr
 115 120 125
 Ala Phe Thr Ile Pro Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr
 130 135 140
 Gln Tyr Asn Val Leu Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe
 145 150 155 160
 Gln Ser Ser Met Thr Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro
 165 170 175
 Asp Ile Val Ile Tyr Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp
 180 185 190
 Leu Glu Ile Gly Gln His Arg Thr Lys Ile Glu Glu Leu Arg Gln His
 195 200 205
 Leu Leu Arg Trp Gly Leu Thr Thr Pro Asp Lys Lys His Gln Lys Glu
 210 215 220
 Pro Pro Phe Leu Trp Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr
 225 230 235 240
 Val Gln Pro Ile Val Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp
 245 250 255
 Ile Gln Lys Leu Val Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro
 260 265 270
 Gly Ile Lys Val Arg Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala
 275 280 285
 Leu Thr Glu Val Ile Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala
 290 295 300
 Glu Asn Arg Glu Ile Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp
 305 310 315 320
 Pro Ser Lys Asp Leu Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln
 325 330 335
 Trp Thr Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
 340 345 350
 Lys Tyr Ala Arg Met Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu
 355 360 365
 Thr Glu Ala Val Gln Lys Ile Thr Thr Glu Ser Ile Val Ile Trp Gly
 370 375 380
 Lys Thr Pro Lys Phe Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Thr
 385 390 395 400
 Trp Trp Thr Glu Tyr Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe
 405 410 415
 Val Asn Thr Pro Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu
 420 425 430
 Pro Ile Val Gly Ala Glu Thr Phe
 435 440

<210> 6
 <211> 170
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 6
 Lys Glu Gly His Gln Met Lys Glu Cys Thr Glu Arg Gln Ala Asn Phe
 1 5 10 15
 Leu Gly Lys Ile Trp Pro Ser His Lys Gly Arg Pro Gly Asn Phe Leu
 20 25 30

Gln Ser Arg Pro Glu Pro Thr Ala Pro Pro Glu Glu Ser Phe Arg Cys
 35 40 45
 Gly Glu Glu Lys Thr Thr Pro Pro Gln Lys Pro Glu Gln Thr Asp Lys
 50 55 60
 Glu Leu Tyr Pro Leu Ala Ser Leu Arg Ser Leu Phe Gly Gln Arg Pro
 65 70 75 80
 Leu Val Thr Ile Lys Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu Asp
 85 90 95
 Thr Gly Ala Asp Asp Thr Val Leu Glu Asp Met Ser Leu Pro Gly Lys
 100 105 110
 Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val Arg
 115 120 125
 Gln Tyr Asp Gln Ile Pro Ile Glu Ile Cys Gly His Lys Ala Ile Gly
 130 135 140
 Thr Val Leu Ile Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn Leu
 145 150 155 160
 Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe
 165 170

<210> 7
 <211> 511
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 7
 aaaggaaagga caccaaatga aagaatgcac ttagagagacag gctaattttt tagggaaaat 60
 ctggccttcc cacaaggaa ggcgcaggaa ctttctccag agcagaccag agccaaacagc 120
 cccaccagaa gagagcttca ggtgtgggaa ggagaaaaaca actccccctc agaagccgga 180
 gcagacagac aaggaaactgt atcccttagc ttccctcaga tcactctttg gcaacgaccc 240
 ctcgtcaca aaaaatagg ggggcagcta aaggaagctc tattagatac aggagcagat 300
 gatacagtat tagaagacat gagtttgcca gggaaaatggg aagccaaaaat gataggggg 360
 attggagggtt ttatcaaagt aagacagtat gatcagatac ctatagaaat ctgtgggcat 420
 aaagctata gta cacttattt aataggacca acacctgtca acataattgg aagaaaatctg 480
 ttgacacaga ttgggtgcac tttaaatttt c 511

<210> 8
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<400> 8
 Tyr Met Asp Asp
 1

<210> 9
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence; note =
 synthetic construct

<220>
<221> VARIANT
<222> 2
<223> Xaa = any amino acid

<400> 9
Tyr Xaa Asp Asp
1

<210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 10
aagcccgaaa tggatggccc aaaagt 26

<210> 11
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 11
tcctaaacgc gtctccctct aagctgctca atttacttag aaagt 45

<210> 12
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 12
actttctaaag taaaattgagc agcttagagg gagacgcgtt tagga 45

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 13
tatgtcgaca cccaaattatg aaaag 25

<210> 14
<211> 32
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 14
tagatcagat ctgttgaactc agattggttg ca 32

<210> 15
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 15
atctacacgc'gtttagaagg tttctgcgcc tt 32

<210> 16
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 16
ttattaacgc gtccgccccct ctccctcccc cc 32

<210> 17
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 17
ccatccgggg cttaatttt actggtagac ttcaatagg actaatgggt cccatggat 60
tatcgctt 69

<210> 18
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence; note =
synthetic construct

<400> 18
agcttgcctt gagtgcttca a 21

<210> 19
<211> 26
<212> DNA
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 19

cttgctagaga ttttccacac tgacta

26

<210> 20

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 20

ggcttagctag ggaacccact g

21

<210> 21

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence; note =
synthetic construct

<400> 21

atactgacgc tctcgcaccc at

22